Isomorphism between morphological and functional graphs of the cell and classification of cells by the extensions of graphs

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Morphological and functional graphs of the cell are constructed, expressing dynamic ontogenetic transformations between six different types of membranes of organelles and the interrelations between six different functions of vital significance for the cell. Morphisms (epimorphisms) from different biological graphs to a functional graph are constructed. It is shown that there exists an isomorphism between morphological and functional graphs which expresses the most essential forms of vital processes. It is further shown that the components with vital functions transform and transfer to each other. To classify and construct cell structures the apparatus for extensions of graphs developed by the author is used, which enables hierarchical biological systems to be described.

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The present work concerns an attempt to express some basic phenomena occurring in a cell by means of graphs. N. Rashevsky [1, 2] suggested the construction of an oriented graph for every organism. The graphs corresponding to different organisms are formed from each other with the help of the general rule of geometrical transformation and can be mapped onto each other epimorphously preserving some basic relations.

To some extent our work is close to Rashevsky’s works. We shall try to construct functional and morphological (referring to ontogenetic mutually transformed membranes of organelles) graphs of the cell. We wish to prove that between functional and morphological graphs there is isomorphism expressing the most essential features of vital processes. In the future, similar graphs will make it possible to consider the organization of biological processes in a cell in a different way, to find those forms of order which are not revealed at the present stage. It is natural to try to apply different constructions of the theory of graphs to construct biological structures (see [3] for an example where the apparatus of the extension of graphs is used).

Consider a graph G viewed intuitively as an encoding of a system consisting of objects labelled v and various interrelations between them labelled i.

Being a graph implies that G the set of its vertices, and I, the set of its arrows, are given. Moreover each arrow from I to V has a source and a target from V. In other words G is determined by two sets V, I and two mappings from I to V.

’source’, ‘target’ : I \rightarrow V

such that any arrows having the same source and the same target are the same.

Furthermore let \((G_i)_{v \in V_i}\) be a family of graphs, one for each vertex of G.

An extension of the graph G, with the family \((G_i)_{v \in V_i}\) is a graph H together with an epimorphism \(\sigma:H \rightarrow G\) (epimorphism \(\sigma:V_H \rightarrow V_G\) such that images of incident vertices are either incident or equal), such that \(\sigma(i)=G_i\), for each \(v \in V_G\). An extension \((H,\sigma)\) and family of epimorphisms \(\sigma'(v) \rightarrow G\), determines a certain partial morphism:

\[
f: \prod_{v \in V_G} I_o \rightarrow \prod_{v \in V_G} 2^{V_G},
\]

such that \(f(v^a, i) = 2^{v^a}\), where: \(i \in I_o, v^a \in V_G, a=1,...,n; v^a\)

is a source of the arrow \(i\) and \(v^a\) is the target of the arrow \(i\), \(n\) is the number of vertices in \(f^{-1}(v)\).

To make the notion of graph extension more understandable, let us turn to a particular example: consider the graph G in fig.1a, whose vertices represent two objects \(v_1\) and \(v_2\) and two interrelations, labelled, respectively, \(i_1\) and \(i_2\), incidence for \(i_1\) being from \(v_1\) to \(v_2\) and that for \(i_2\) being

\[
\begin{align*}
&v_1 \\
&\begin{array}{c}
\circ \\
&i_1 \\
&\downarrow \\
&i_2 \\
&v_2
\end{array}
\end{align*}
\]

Figure 1 a. Graph G.

from \(v_2\) to \(v_1\). That is, \(i_1\) begins in \(v_1\) and ends in \(v_2\), and \(i_2\) begins in \(v_2\) and ends in \(v_1\).

We next turn to the definition of a morphism between graphs, say, a morphism from a graph \(G_1\) (fig. 1b) to a graph \(G_2\) (fig. 1c). Let us assign to the vertex \(v_1^1\) of the graph \(G_1\), the vertex \(v_1^2\) of the graph \(G_2\): \(v_1^1 \rightarrow v_1^2\).

In general, a morphism \(f\) of graphs \(G_1\rightarrow G_2\) is a mapping \(f : V_0 \rightarrow V_0\) such that if there is an arrow with source \(v\) and target \(v'\), then either \(f(v)=f(v')\) or there is an arrow with source \(f(v)\) and target \(f(v')\).

If the vertex \(v_1^1\) of the graph \(G_1\) is assigned to the vertex \(v_1^2\) of the graph \(G_2\), then the arrow \(i_1^1\) corresponds to the arrow \(i_1^2\). Hence we obtain a morphism of graphs \(f\) with

\[
f(v_1^2) = v_1^1, f(i_2^1) = i_2^2.
\]
Now what is the definition of an epimorphism from a graph $G_i$ to the graph $G_j$. Intuitively, this means that each vertex of $G_j$ is the image of some vertex from $G_i$.

The map $f$ above is an example of a map which is not an epimorphism, since the vertex $v_1^3$ of $G_i$ has empty inverse images under $f$.

On the other hand, define another map $g$ from the graph $G_i$ to the graph $G_i$ by $v_1^2 → v_1^1$, i.e. by assigning to the vertex $v_1^2$ the vertex $v_1^1$, and furthermore $v_1^2 → v_1^1$; one can check easily that this is a graph morphism which is an epimorphism (see figs 1b and 1c).

Let us now define an extension of a graph $G$ by a family $G_i$ of graphs. For simplicity let us assume that the family $G_{v_1}$, $G_{v_2}$ consists of two graphs $G_i$ and $G_j$. Then, construct a graph $H$ as follows: place at each vertex of $G$ the corresponding graph from the family, i.e. in our case place at the vertex $v_1$ the graph $G_i$, and at $v_2$ the graph $G_j$. Then construct the new arrow $h$ starting at some vertex of $G_i$ and ending in $G_j$, and starting at some vertex $G_j$ and ending in $G_i$ (see Fig. 1d).

Let us show that there is an epimorphism from $H$ to $G$. Indeed, define the map $\sigma$ by $\sigma(G_i) = v_1$, $\sigma(G_j) = v_2$, and $\sigma(h) = i_1$, $\sigma(h) = i_2$, then clearly $\sigma$ is such an epimorphism.

In the language of system theory, $H$ is a compound system consisting of two subsystems $G_i$ and $G_j$, interrelated via $h_1$ and $h_2$, whereas considered as units, they are interrelated via the arrow $i$. The arrow $i$ encodes in itself multiple interrelations, in our particular example two interrelations $h_1$ and $h_2$. In principle this is a mathematical description of the concept of decomposing a whole into interrelated parts.

Such extensions are naturally realized in the following way: as $G$ we take the graph $G_{en}$ corresponding to the relation of exocytosis and endocytosis of the cell (fig. 2a) and with the corresponding $G_{ex}$, $G_{en}$ (figs 2b and 2c) and $f$

Let us now consider the family of mem, i.e. graph $A$ in our earlier work [4]. We can say that instead of vertices expressing endocytosis and exocytosis in the graph $G_{cell}$ we substitute their corresponding graphs $G_{mem}$ and $G_{ex}$ and construct new arrows, the sources of which will be some vertices $v \in G_{mem}$ or $v \in G_{ex}$ and the targets will be some vertices $v \in G_{mem}$ or $v \in G_{ex}$. In its turn graph $G_{mem}$, i.e. graph $G_{ex}$ can also be extended if we know the corresponding graphs for each membrane. It should be noted that the graph which is being extended is hierarchically at a higher level than the graph obtained after extension, i.e. if some graph expresses relations between different components at some level, then after its extension we get the graph expressing relations between the subcomponents of these components at a lower level. Thus, different cellular types are characterized by mappings of the extension $f$, i.e. the cells are marked and coded with different mappings of the extension. Of course not all graphs $G_i$ constructed by different $f$ will correspond to cells. For example, with some $f$’s such graphs $G_i$ are obtained which are trees: and there are 1540944 non-isomorphic oriented 6-vertex graphs altogether (6- orgraphs) [5]. From this number 6 trees and 1296 marked trees must be subtracted. The same could be said about simple orgraphs. After extension of graph $G_{cell}$ by graphs $G_{mem}$ and $G_{ex}$ and the two mappings $f$ and $g$, the extended graphs $G_{mem}$ and $G_{ex}$ may happen to be isomorphic. The isomorphism between $G_{mem}$ and $G_{ex}$, i.e. the equivalence between mappings, is tested in the following way:

$$g(T(v,i)) = T[f(v,i)].$$

where $i \in I$, $v \in V_{G_i}$, and $T$ is the automorphism of the family $(G_{v_1}, v_1)$. 

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**Figure 1 a.** Graph $G_{en}$.

**Figure 1 b.** Graph $G_i$.

**Figure 1 c.** Graph $G_j$.

**Figure 1 d.** Graph $H$.

**Figure 2.** From top to bottom:

a) the graph $G_{en}$ corresponding to the relation of exocytosis and endocytosis of the cell;

b) the graph $G_{ex}$ expressing endocytosis of the cell;

c) the graph $G_{en}$ expressing exocytosis of the cell.
Let us illustrate the above by an example. Let the graph $G_0$ be given (fig. 2a). Let also graphs $G_n$ and $G_m$ be given (fig. 2b and 2c). Let the mappings of extension $f$ and $g$ be given, defined in the following way:

$$f(v_{ex1},i_{ex1})=\{v_{en1}\}; \quad g(v_{en1},i_{en1})=\{v_{en2}\}$$

$$f(v_{ex2},i_{ex2})=\{v_{en2}\}; \quad g(v_{en2},i_{en2})=\{v_{en3}\}$$

Let us construct the extensions $G_f$ and $G_g$ of the graph $G_0$ by graphs $G_n$ and $G_m$ and the mappings $f$ and $g$. If we apply the equality (2) then $G_f$ and $G_g$ will be isomorphic (fig. 3).

Thus, after extension of the graph $G_0$ by graphs $G_n$ and $G_m$ and the equivalent mappings of $f$ and $g$ we obtain isomorphic graphs $G_f$ and $G_g$ representing the same cell. Now our primary task is the construction of graph $A$, i.e. graph $G_{non}$, as described in the next section.

**Construction of the graph of ontogenetic transformations of membranes of organelles - the morphological graph $A$ (the graph $G_{non}$)**

In modelling a cell (as well as in modelling any system) it is necessary to define the most essential features, and this may be done with a block-scheme. From common theoretical, mathematical, cybernetical etc. considerations we have described such a block-scheme [4],[6-8].

We assume that in a cell there is a such a dynamical composition which covers the relations between membranes and expresses the functional morphology of the cell. Many biological processes occurring in the cell rest upon this composition as the basis. The relations between various membranes can be expressed by a graph showing the dynamics of morphological transformations in ontogenesis [4],[6-8]. This graph is the morphological block-scheme of the cell (fig.4). The vertices of graph $A$ denote membranes and the arrows denote mutual transformations of membranes in ontogenesis. These arrows are constructed on the basis of data from different authors; for example, refs [9-13] were used to construct the arrow from the Golgi complex to the plasmalemma. For the non-biologist reader we’ll try to make more explicit the membranes, their intertransformations and biogenesis. Biological membranes are lipid-protein complexes in which the lipid molecules form an ordered (liquid-crystallic) layer, in which the protein molecules are inserted. Topologically, membrane surfaces are closed two-dimensional oriented (two-sided) surfaces. The two sides (inner and outer) bounding this layer differ from each other significantly. Discontinuities of biological membranes, with the formation of free boundaries, vanish practically instantaneously by “annealing”, with recovering of continuity of the membrane surface. The surface of each cell is covered by the plasma (outer) membrane. For the simplest cells (prokaryota) this is the only membrane system. Topologically, it is a sphere surface.

In cells of higher type (eukaryota) the inner cell membrane systems are very variable both morphologically and functionally. The membrane systems of eukaryotic cells are closed surfaces (membranic organoids) of various topological genus, which are embedded into the closed surfaces formed by the plasma membranes, i.e. into spheres. Moreover, most of the vital processes of a cell are related to membranes. In order to understand the morphofunctional organization of the cell, consideration of the dynamics of membrane transformations—topological transformations of surfaces formed by membranes—is most important.

Among the most complicated of these systems is the outer membrane of the nucleus, which is topologically a sphere, i.e. a sphere embedded into another one. The outer membrane of the nucleus consists of membrane surfaces of two types, which are related to each other by channels (holes piercing the membrane). Since the number of holes is very high, the genus of the surface of the nucleus is very high too. Moreover the number of holes varies according to various functional activities.

Bubbles (small spheres), or fragments with holes, continuously separate from the outer nuclear surface. Furthermore, these small bubbles form, by coalescence, surfaces of other types, in particular the endoplasmic reticulum. Hence, topological transformations of the nuclear membrane take place continuously—both its genus and connectivity changes.

Topologically, membrane circulation is the process of change of membrane connectivity—i.e. when some parts...
become cut out and the cutouts closed up by spheres, and simultaneously free boundaries of membranes become glued in. In their turn, small membrane spheres again coalesce with each other and newly formed bubbles become inserted in the membrane of the plasmalemma. Thus the bubbles separated from the Golgi complex form the plasmalemma, i.e. a membrane surface of one type (the Golgi surface) forms a membrane surface of another type (the plasmalemma).

Similar facts hold concerning the interrelations of pairs of other membrane surfaces. Their topological differences determine functional differences, whereas topological intertransformations relate the functionalities of membrane-based organelles of different types, and the possibility of their realization is a necessary condition for the functioning of the synthetic and transportational succession of the cell.

The construction of the functional graph $D$

Functions of vital importance take place in the cell: the reception (assimilation) of food and energy, the decomposition and synthesis of new substances, and their storage and excretion. In the work [4] the list of functions did not include the transport of nuclear metabolites; it is now included. These functions are interrelated in such a way that they form the administrative contour of the cell. To support life as a whole it is necessary to have the way that they form the administrative contour of the cell. Now we can give a positive answer to this question. The six mutually related functions performed by those membranes which are reconstructed in ontogenesis are the cause, i.e. the mechanism, of the reconstruction. $v_{ex_1}$, $v_{en_1}$ is the nuclear membrane, $v_{en_2}$ is the endoplasmic reticulum, $v_{en_3}$ is the residual body, $v_{ex_2}$ is the lysosome, $v_{ex_3}$ is the plasmalemma, $v_{en_4}$ is the Golgi complex. Ontogenetic intertransformations of the membranes of the cell are characterized by this mapping $f$ (fig. 4).

If the second mapping $g$ is also given and if $G_r$ and $G_e$ are the graphs of the cell, then with the help of the equality (2) we can predict whether the graphs $G_r$ and $G_e$ will be the graphs of the same cell, or of different cells.

Finally we can note that construction of a graph of a complex biological organism from a simple (primordial) graph in Rashevsky’s work is virtually an extension too, although in his works the word extension is never mentioned [1, 2].

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Figure 5. The functional graph $D$.
REFERENCES